

## SEQUENCE LISTING

<110> TOYO BOSEKI KABUSHIKI KAISHA

<120> MODIFIED THERMOSTABLE DNA POLYMERASE

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<150> 2000-138796

<151> 2000-05-11

<160> 28

<170> PatentIn Ver. 2.1

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<211> 5342

<212> DNA

<213> Pyrococcus kodakaraensis

<220>

<221> CDS

<222> (156)..(5165)

<223> 1374-2453 intron, 2709-4316 intron

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ataacggaga aaaatgggga gctattacga tctctccttg atgtgggggt tacaataaag 120

cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac 173

09852922.051004

Met Ile Leu Asp Thr Asp

1

5

tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221

Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu

10

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20

aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269

Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe

25

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35

tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317

Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile

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acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365

Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys

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70

gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413

Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr

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ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461

Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu

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90	95	100	
cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag			509
His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys			
105	110	115	
cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag			557
Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu			
120	125	130	
ctg aaa atg ctc gcc ttc gac att gaa act ctc tac cat gag ggc gag			605
Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu			
135	140	145	150
gag ttc gcc gag ggg cca atc ctt atg ata agc tac gcc gac gag gaa			653
Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu			
155	160	165	
ggg gcc agg gtg ata act tgg aag aac gtg gat ctc ccc tac gtt gac			701
Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp			
170	175	180	
gtc gtc tcg acg gag agg gag atg ata aag cgc ttc ctc cgt gtt gtg			749
Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val			
185	190	195	

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295                      300                      305                      310

315                      320                      325

330                      335                      340

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375                      380                      385                      390

gag ccc gag aga ggg ttg tgg gag aac ata gtg tac cta gat ttt aga 1373

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420

435

450

470

485

Ser Phe Leu Thr Lys Lys Val Lys Gly Lys Ile Ile Thr Thr Pro Leu

490	495	500	
ttc tat gaa ata ggc aga gcg aca agt gag aat att cca gaa gaa gag			1709
Phe Tyr Glu Ile Gly Arg Ala Thr Ser Glu Asn Ile Pro Glu Glu Glu			
505	510	515	
gtt ctc aag gga gag ctc gct ggc ata cta ttg gct gaa gga acg ctc			1757
Val Leu Lys Gly Glu Leu Ala Gly Ile Leu Leu Ala Glu Gly Thr Leu			
520	525	530	
ttg agg aaa gac gtt gaa tac ttt gat tca tcc cgc aaa aaa cgg agg			1805
Leu Arg Lys Asp Val Glu Tyr Phe Asp Ser Ser Arg Lys Lys Arg Arg			
535	540	545	550
att tca cac cag tat cgt gtt gag ata acc att ggg aaa gac gag gag			1853
Ile Ser His Gln Tyr Arg Val Glu Ile Thr Ile Gly Lys Asp Glu Glu			
555	560	565	
gag ttt agg gat cgt atc aca tac att ttt gag cgt ttg ttt ggg att			1901
Glu Phe Arg Asp Arg Ile Thr Tyr Ile Phe Glu Arg Leu Phe Gly Ile			
570	575	580	
act cca agc atc tcg gag aag aaa gga act aac gca gta aca ctc aaa			1949
Thr Pro Ser Ile Ser Glu Lys Lys Gly Thr Asn Ala Val Thr Leu Lys			
585	590	595	

09852922-051001

gtt gcg aag aag aat gtt tat ctt aaa gtc aag gaa att atg gac aac 1997

Val Ala Lys Lys Asn Val Tyr Leu Lys Val Lys Glu Ile Met Asp Asn

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610

ata gag tcc cta cat gcc ccc tcg gtt ctc agg gga ttc ttc gaa ggc 2045

Ile Glu Ser Leu His Ala Pro Ser Val Leu Arg Gly Phe Phe Glu Gly

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625

630

gac ggt tca gta aac agg gtt agg agg agt att gtt gca acc cag ggt 2093

Asp Gly Ser Val Asn Arg Val Arg Arg Ser Ile Val Ala Thr Gln Gly

635

640

645

aca aag aac gag tgg aag att aaa ctg gtg tca aaa ctg ctc tcc cag 2141

Thr Lys Asn Glu Trp Lys Ile Lys Leu Val Ser Lys Leu Leu Ser Gln

650

655

660

ctt ggt atc cct cat caa acg tac acg tat cag tat cag gaa aat ggg 2189

Leu Gly Ile Pro His Gln Thr Tyr Thr Tyr Gln Tyr Gln Glu Asn Gly

665

670

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aaa gat cgg agc agg tat ata ctg gag ata act gga aag gac gga ttg 2237

Lys Asp Arg Ser Arg Tyr Ile Leu Glu Ile Thr Gly Lys Asp Gly Leu

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685

690

09852922.051001



ata ctg ttc caa aca ctc att gga ttc atc agt gaa aga aag aac gct 2285

Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala

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705

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ctg ctt aat aag gca ata tct cag agg gaa atg aac aac ttg gaa aac 2333

Leu Leu Asn Lys Ala Ile Ser Gln Arg Glu Met Asn Asn Leu Glu Asn

715

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725

aat gga ttt tac agg ctc agt gaa ttc aat gtc agc acg gaa tac tat 2381

Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr

730

735

740

gag ggc aag gtc tat gac tta act ctt gaa gga act ccc tac tac ttt 2429

Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe

745

750

755

gcc aat ggc ata ttg acc cat aac tcc ctg tac ccc tca atc atc atc 2477

Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile

760

765

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acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa 2525

Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu

775

780

785

790

tat gac gtt gcc cca cag gtc ggc cac cgc ttc tgc aag gac ttc cca 2573

T00T50" 22625860

Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro

795

800

805

gga ttt atc ccg agc ctg ctt gga gac ctc cta gag gag agg cag aag 2621

Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys

810

815

820

ata aag aag aag atg aag gcc acg att gac ccg atc gag agg aag ctc 2669

Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu

825

830

835

ctc gat tac agg cag agg gcc atc aag atc ctg gca aac agc atc cta 2717

Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu

840

845

850

ccc gag gaa tgg ctt cca gtc ctc gag gaa ggg gag gtt cac ttc gtc 2765

Pro Glu Glu Trp Leu Pro Val Leu Glu Glu Gly Glu Val His Phe Val

855

860

865

870

agg att gga gag ctc ata gac cgg atg atg gag gaa aat gct ggg aaa 2813

Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys

875

880

885

gta aag aga gag ggc gag acg gaa gtg ctt gag gtc agt ggg ctt gaa 2861

Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu

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gtc ccg tcc ttt aac agg aga act aac aag gcc gag ctc aag aga gta			2909
Val Pro Ser Phe Asn Arg Arg Thr Asn Lys Ala Glu Leu Lys Arg Val			
905	910	915	
aag gcc ctg att agg cac gat tat tct ggc aag gtc tac acc atc aga			2957
Lys Ala Leu Ile Arg His Asp Tyr Ser Gly Lys Val Tyr Thr Ile Arg			
920	925	930	
ctg aag tcg ggg agg aga ata aag ata acc tct ggc cac agc ctc ttc			3005
Leu Lys Ser Gly Arg Arg Ile Lys Ile Thr Ser Gly His Ser Leu Phe			
935	940	945	950
tct gtg aga aac ggg gag ctc gtt gaa gtt acg ggc gat gaa cta aag			3053
Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys			
955	960	965	
cca ggt gac ctc gtt gca gtc ccg cgg aga ttg gag ctt cct gag aga			3101
Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg			
970	975	980	
aac cac gtg ctg aac ctc gtt gaa ctg ctc ctt gga acg cca gaa gaa			3149
Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu			
985	990	995	

09852932 051001

gaa act ttg gac atc gtc atg acg atc cca gtc aag ggt aag aag aac 3197

Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn

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1005

1010

ttc ttt aaa ggg atg ctc agg act ttg cgc tgg att ttc gga gag gaa 3245

Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu

1015

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aag agg ccc aga acc gcg aga cgc tat ctc agg cac ctt gag gat ctg 3293

Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu

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ggc tat gtc cgg ctt aag aag atc ggc tac gaa gtc ctc gac tgg gac 3341

Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp

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tca ctt aag aac tac aga agg ctc tac gag gcg ctt gtc gag aac gtc 3389

Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val

1065

1070

1075

aga tac aac ggc aac aag agg gag tac ctc gtt gaa ttc aat tcc atc 3437

Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile

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cgg gat gca gtt ggc ata atg ccc cta aaa gag ctg aag gag tgg aag 3485

Arg Asp Ala Val Gly Ile Met Pro Leu Lys Glu Leu Lys Glu Trp Lys

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1100

1105

1110

atc ggc acg ctg aac ggc ttc aga atg aga aag ctc att gaa gtg gac 3533

Ile Gly Thr Leu Asn Gly Phe Arg Met Arg Lys Leu Ile Glu Val Asp

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1125

gag tcg tta gca aag ctc ctc ggc tac tac gtg agc gag ggc tat gca 3581

Glu Ser Leu Ala Lys Leu Leu Gly Tyr Tyr Val Ser Glu Gly Tyr Ala

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aga aag cag agg aat ccc aaa aac ggc tgg agc tac agc gtg aag ctc 3629

Arg Lys Gln Arg Asn Pro Lys Asn Gly Trp Ser Tyr Ser Val Lys Leu

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1150

1155

tac aac gaa gac cct gaa gtg ctg gac gat atg gag aga ctc gcc agc 3677

Tyr Asn Glu Asp Pro Glu Val Leu Asp Asp Met Glu Arg Leu Ala Ser

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1165

1170

agg ttt ttc ggg aag gtg agg cgg ggc agg aac tac gtt gag ata ccg 3725

Arg Phe Phe Gly Lys Val Arg Arg Gly Arg Asn Tyr Val Glu Ile Pro

1175

1180

1185

1190

aag aag atc ggc tac ctg ctc ttt gag aac atg tgc ggt gtc cta gcg 3773

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Lys Lys Ile Gly Tyr Leu Leu Phe Glu Asn Met Cys Gly Val Leu Ala

1195

1200

1205

gag aac aag agg att ccc gag ttc gtc ttc acg tcc ccg aaa ggg gtt 3821

Glu Asn Lys Arg Ile Pro Glu Phe Val Phe Thr Ser Pro Lys Gly Val

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1215

1220

cgg ctg gcc ttc ctt gag ggg tac tca tcg gcg atg gcg acg tcc acc 3869

Arg Leu Ala Phe Leu Glu Gly Tyr Ser Ser Ala Met Ala Thr Ser Thr

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gaa caa gag act cag gct ctc aac gaa aag cga gct tta gcg aac cag 3917

Glu Gln Glu Thr Gln Ala Leu Asn Glu Lys Arg Ala Leu Ala Asn Gln

1240

1245

1250

ctc gtc ctc ctc ttg aac tcg gtg ggg gtc tct gct gta aaa ctt ggg 3965

Leu Val Leu Leu Leu Asn Ser Val Gly Val Ser Ala Val Lys Leu Gly

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1265

1270

cac gac agc ggc gtt tac agg gtc tat ata aac gag gag ctc ccg ttc 4013

His Asp Ser Gly Val Tyr Arg Val Tyr Ile Asn Glu Glu Leu Pro Phe

1275

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1285

gta aag ctg gac aag aaa aag aac gcc tac tac tca cac gtg atc ccc 4061

Val Lys Leu Asp Lys Lys Lys Asn Ala Tyr Tyr Ser His Val Ile Pro

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1300

Lys Glu Val Leu Ser Glu Val Phe Gly Lys Val Phe Gln Lys Asn Val

1315

Ser Pro Gln Thr Phe Arg Lys Met Val Glu Asp Gly Arg Leu Asp Pro

1330

Glu Lys Ala Gln Arg Leu Ser Trp Leu Ile Glu Gly Asp Val Val Leu

1350

Asp Arg Val Glu Ser Val Asp Val Glu Asp Tyr Asp Gly Tyr Val Tyr

1365

Asp Leu Ser Val Glu Asp Asn Glu Asn Phe Leu Val Gly Phe Gly Leu

1380

Val Tyr Ala His Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Arg Ala

1395

1410

1430

1445

1460

1475

1490



gag gaa ggc aag ata aca acg cgc gga ctt gag att gtg agg cgt gac 4685

Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu Glu Ile Val Arg Arg Asp

1495

1500

1505

1510

tgg agc gag ata gcg aaa gag acg cag gcg agg gtt ctt gaa gct ttg 4733

Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Ala Leu

1515

1520

1525

cta aag gac ggt gac gtc gag aag gcc gtg agg ata gtc aaa gaa gtt 4781

Leu Lys Asp Gly Asp Val Glu Lys Ala Val Arg Ile Val Lys Glu Val

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1535

1540

acc gaa aag ctg agc aag tac gag gtt ccg ccg gag aag ctg gtg atc 4829

Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro Pro Glu Lys Leu Val Ile

1545

1550

1555

cac gag cag ata acg agg gat tta aag gac tac aag gca acc ggt ccc 4877

His Glu Gln Ile Thr Arg Asp Leu Lys Asp Tyr Lys Ala Thr Gly Pro

1560

1565

1570

cac gtt gcc gtt gcc aag agg ttg gcc gcg aga gga gtc aaa ata cgc 4925

His Val Ala Val Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Ile Arg

1575

1580

1585

1590

cct gga acg gtg ata agc tac atc gtg ctc aag ggc tct ggg agg ata 4973

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Pro Gly Thr Val Ile Ser Tyr Ile Val Leu Lys Gly Ser Gly Arg Ile

1595

1600

1605

ggc gac agg gcg ata ccg ttc gac gag ttc gac ccg acg aag cac aag 5021

Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe Asp Pro Thr Lys His Lys

1610

1615

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tac gac gcc gag tac tac att gag aac cag gtt ctc cca gcc gtt gag 5069

Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Glu

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aga att ctg aga gcc ttc ggt tac cgc aag gaa gac ctg cgc tac cag 5117

Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln

1640

1645

1650

aag acg aga cag gtt ggt ttg agt gct tgg ctg aag ccg aag gga act 5165

Lys Thr Arg Gln Val Gly Leu Ser Ala Trp Leu Lys Pro Lys Gly Thr

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tgacctttcc atttgttttc cagcggataa cccitttaact tccctttcaa aaactccctt 5225

tagggaaaga ccatgaagat agaaatccgg cggcgcccgg ttaaatacgc taggatagaa 5285

gtgaagccag acggcaggt agtcgtcact gccccgaggg ttcaacgttg agaagtt 5342

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&lt;211&gt; 774

&lt;212&gt; PRT

<213> *Pyrococcus kodakaraensis*

&lt;400&gt; 2

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1

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15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg

20

25

30

Thr Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile

35

40

45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Val Val Thr

50

55

60

Val Lys Arg Val Glu Lys Val Gln Lys Lys Phe Leu Gly Arg Pro Val

65

70

75

80

Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile

85

90

95

09852922-051001

Arg Asp Lys Ile Arg Glu His Pro Ala Val Ile Asp Ile Tyr Glu Tyr

100

105

110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro

115

120

125

Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr

130

135

140

Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile

145

150

155

160

Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Val

165

170

175

Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Arg Glu Met Ile Lys

180

185

190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

195

200

205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

210

215

220

Lys Leu Gly Ile Asn Phe Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys

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225                                      230                                      235                                      240

Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile

245                                      250                                      255

His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr

260                                      265                                      270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu

275                                      280                                      285

Lys Val Tyr Ala Glu Glu Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn

290                                      295                                      300

Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr

305                                      310                                      315                                      320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu

325                                      330                                      335

Ile Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu

340                                      345                                      350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala

355                                      360                                      365

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Pro Asn Lys Pro Asp Glu Lys Glu Leu Ala Arg Arg Arg Gln Ser Tyr

370

375

380

Glu Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile

385

390

395

400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His

405

410

415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr Asp

420

425

430

Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro Gly Phe

435

440

445

Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Ile Lys

450

455

460

Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu Leu Asp

465

470

475

480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr

485

490

495

00852922.051001

Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser

500

505

510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Thr Met Thr Ile Lys Glu Ile

515

520

525

Glu Glu Lys Tyr Gly Phe Lys Val Ile Tyr Ser Asp Thr Asp Gly Phe

530

535

540

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

Met Glu Phe Leu Lys Tyr Ile Asn Ala Lys Leu Pro Gly Ala Leu Glu

565

570

575

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu

595

600

605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

Arg Val Leu Glu Ala Leu Leu Lys Asp Gly Asp Val Glu Lys Ala Val

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625                      630                      635                      640

Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645                      650                      655

Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Asp Leu Lys Asp

660                      665                      670

Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala

675                      680                      685

Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690                      695                      700

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705                      710                      715                      720

Asp Pro Thr Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln

725                      730                      735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

740                      745                      750

Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Ser Ala Trp

755                      760                      765

09852922-051001



Leu Lys Pro Lys Gly Thr

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<210> 3

<211> 2325

<212> DNA

<213> *Pyrococcus kodakaraensis*

<400> 3

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ctcctgaagg acgattctgc cattgaggaa gtcaagaaga taaccgccga gaggcacggg 180  
acggttgtaa cggttaagcg ggttgaaaag gticagaaga agttcctcgg gagaccagtt 240  
gaggcttgga aactctactt tactcatccg caggacgtcc cagcgataag ggacaagata 300  
cgagagcatc cagcagttat tgacatctac gactacgaca tacccttcgc caagcgctac 360  
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attcagagga tgggcgacag gtttgccgtc gaagtgaagg gacggataca ctctgatctc 780  
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09852922-051001

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